

FIG. 1A

1	CCACCGGTCCGGGAGCTTGCACTAACATCTACAATGGCTCTAAAAAGCACAGATGAC	60
61	CTGCTACACTTCCTGACTTGCTTGCATTGGTGGCACTGTTCATAAATATAATTTGCTC	120
121	TTTCACTTTCTTGAAATGAGCAACCTGAATTACTCGGAGGAGAAAGGCAGGAGAGATA	180
181	GAGGCAGCAGAACGCCAGGGCAGCTGAAAGACAGAGACCTTCAGTCTGAACCAACAACAAG	240
241	CAAAGTTAAATTATGGATATCCAAGGGAGTCTATAGAAGGTCCATGCAAGACATTTGAC	300
301	TACTTGTCTGAACTAGATATCCCTTGAATGTGCACACAAAAAGTGAATGGGTCAATTGAT	360
361	AAGGGAAAATAGGTTCCAAGATGGCTGAATAGGAAGAGCTCCAGTCTGCAGATCCCAGT	420
421	GTGAGCAACGTGGAAGATGGGTGATTCTGCATTCCAATGAGCATGGAGAGAAAAATT	480
481	TATGTCCTTGCACCACATCCATCTCCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAA 1 M E P N G T F S N	540 9
541	TAACAAACAGCAGGAACACTGCACAATTGAAAATTCAAGAGAGAATTTCCTCAATTGTATA 10 N N S R N C T I E N F K R E F F P I V Y	600 29
601	TCTGATAATATTTCTGGGGAGTCTTGGGAAATGGGTGTCCATATATGTTTCCTGCA 30 L I I F F W G V L G N G L S I Y V F L Q	660 49
661	GCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAATCTGCCATTTCAGATCT 50 P Y K K S T S V N V F M L N L A I S D L	720 69
721	CCTGTTCATAGCACGCTTCCCTCAGGGCTGACTATTATCTTAGAGGGCTCCAATTGGAT 70 L F I S T L P F R A D Y Y L R G S N W I	780 89
781	ATTTGGAGACCTGGCCTGCAGGATTATGTCTTATTCTTGATGTCAACATGTACAGCAG 90 F G D L A C R I M S Y S L Y V N M Y S S	840 109
841	TATTTATTCCTGACCGTGCTGAGTGTGCGTTCTGGCAATGGTCACCCCTTTCG 110 I Y F L T V L S V V R F L A M V H P F R	900 129

FIG. 1B

FIG. 2A

HGPRBMY11 HGPRBMY11v1 P2Y5_CHICK P2YR_CHICK P2YR_MELGA P2YR_RAT Q9Y271 GPRH_HUMAN	1 (1) -----MSLQPSI[FVSE]EPNG-----TFINNSRNCEEN--FL (1) MERKFM[SLQPSI[FVSE]EPNG-----TFINNSRNCEEN--FL (1) ----- (1) MTEALISAALNG[QOPEN]LAGG-----WAICNA[TKC]TKTGFN (1) MTEALISAALNG[QOPEN]LAGG-----WAICNA[TKC]TKTGFN (1) MTEVPWSAVPNG[DAA]LAGLGLSLWGNSTIASA[VENSFRCEVIKTGFN (1) -----MDETG-----NLTV[SAT]CHDTIDDFE (1) -----MNGL[EAPP-----LITNFSLIAEQ[GQETP]	50
HGPRBMY11 HGPRBMY11v1 P2Y5_CHICK P2YR_CHICK P2YR_MELGA P2YR_RAT Q9Y271 GPRH_HUMAN	51 (22) REEFPIIVYIKFFEWGVLGNC[GSI]VFE[PON]KS[RE]VVMENLA[SDLLK] (38) REEFPIIVYIKFFEWGVLGNC[GSI]VFE[PON]KS[RE]VVMENLA[SDLLK] (14) VTE[GEVESMVFWF]GFLGN[VAI]VMPVHME[PWS]VYVYMENLA[ADELV] (40) YYVTP[IVYILVFI]GFLGN[VAI]VMPVHME[PWS]VYVYMENLA[ADELV] (40) YYVTP[IVYILVFI]GFLGN[VAI]VMPVHME[PWS]VYVYMENLA[ADELV] (51) YYVTP[IVYILVFI]GFLGN[VAI]VMPVHME[PWS]VYVYMENLA[ADELV] (23) NOVYSTLYSMESIVGFFGNGFV[EYAGK]TVEKKSA[RGVY]MENLA[ADLLC] (31) NM[LEAS]FVYILD[FIAV]GN[PA]WFE[ERDH]SGFP[ON]VMA[VL]AMADLSC	100
HGPRBMY11 HGPRBMY11v1 P2Y5_CHICK P2YR_CHICK P2YR_MELGA P2YR_RAT Q9Y271 GPRH_HUMAN	101 (72) E[STL]PFRADYYERGS[NWIFGD]ACKR[MS]S[VNV]MYS[SI]YFLTV[SVV]RF (88) E[STL]PFRADYYERGS[NWIFGD]ACKR[MS]S[VNV]MYS[SI]YFLTV[SVV]RF (64) V[TL]LFRIYYEVV[EN-WPFGD]V[C]KLSV[TFY]MMYGSILFLTCISVDRF (90) VLTLFA[LIEYYFN]KTDWIFGD[V]CKLQR[TFHVN]YGSILFLTCISVHRY (90) VLTLFA[LIEYYFN]KTDWIFGD[V]CKLQR[TFHVN]YGSILFLTCISVHRY (101) VLTLFA[LIEYYFN]KTDWIFGD[V]CKLQR[TFHVN]YGSILFLTCISAHRY (73) V[CTLP]L[RVV]VYVHKGIWLF[GDF]C[R]ST[V]MAYV[V]YCSIEFMTAMSSFFRC (81) V[LM]LP[TR]L[VYHFS]GN[HWP]FGE[A]C[R]TC[E]FYIENMYASIYFLTCISADR	150
HGPRBMY11 HGPRBMY11v1 P2Y5_CHICK P2YR_CHICK P2YR_MELGA P2YR_RAT Q9Y271 GPRH_HUMAN	151 (122) LAMVHP[ELLHYTS]ISRAWIFCGE[W]L[EN]ASSIMILDS---GSEONGSV (138) LAMVHP[ELLHYTS]ISRAWIFCGE[W]L[EN]ASSIMILDS---GSEONGSV (113) LAIVVHP[RSK]TUR[KRNAR]IVCVVA[VI]TVIAGSIPASFQ[ST]NRQNTEQ (140) TGVVHP[KL]SLGREKKNAV[V]S[V]VWVAVIA[PH]FVSGTGV[R]ANKTH (140) TGVVHP[KL]SLGREKKNAV[V]S[V]VWVAVIA[PH]FVSGTGV[R]ANKTH (151) SGVYV[FL]KSLGREKKNAI[V]S[V]VWVAVIA[PH]FVSGT[GIR]NKTV (123) IAIIVF[V]ONINL[V]OKKARF[V]CG[V]W[V]I[V]L[V]SSPEELMAKPQKDEKNNTK (131) LAIVVHP[VKSL]KURRPLY[AH]IAC[FL]W[V]V[V]MAPLLV[S]PQT[V]QT[N]TV	200
HGPRBMY11 HGPRBMY11v1 P2Y5_CHICK P2YR_CHICK P2YR_MELGA P2YR_RAT Q9Y271 GPRH_HUMAN	201 (169) T[SCLE]--LNLYKA[K]Q[DMY]FALVV[GCL]P[P]F[SI]CYLLIIRVLEKVE (185) T[SCLE]--LNLYKA[K]Q[DMY]FALVV[GCL]P[P]F[SI]CYLLIIRVLEKVE (163) RTCFENFP[EST]W[K]TY[SR]I[V]E[I]FVGF[FP]TEN[V]C[ST]W[TR]A[L]NKPL (190) TCYDT--TADE[RSYF]V[WSMC]T[V]FMPC[LP]F[V]T[G]CYGLIV[AL]LYKE (190) TCYDT--TADE[RSYF]V[WSMC]T[V]FMPC[LP]F[V]T[G]CYGLIV[AL]LYKE (201) TCYDS--TSDE[RSYF]V[WSMC]T[V]FMPC[LP]F[V]T[G]CYGLIV[RL]LYKE (173) CFEPP--QDNQTKNH[L]LHY[SL]FVG[II]PP[V]T[V]C[Y]T[II]L[BL]KK (181) CLQLY-----REKA[SHH]A[V]S[V]A[V]F[V]T[V]P[V]T[V]C[Y]LLIIRSLREGI	250

FIG. 6A

1	ATGGAGAGAAAATTATGTCCTTGCAACCATCCATCTCCGTATCAGAAATGGAACCAAAT	60
1	M E R K F M S L Q P S I S V S E M E P N	20
61	GGCACCTTCAGCAATAACAACAGCAGGAACACTGCACAATTGAAAATTCAAGAGAGAATT	120
21	G T F S N N N S R N C T I E N F K R E F	40
121	TTCCCATTGATATCTGATAATATTTCTGGGGAGTCTGGGAAATGGGTGTCCATA	180
41	F P I V Y L I I F F W G V L G N G L S I	60
181	TATGTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTCATGCTAAATCTG	240
61	<u>Y V F L Q P Y K K S T S V N V F M L N L</u>	80
241	GCCATTCAGATCTCCTGTTCAAAAGCACGCTCCCTCAGGGCTGACTATTATCTTAGA	300
81	<u>A I S D L L F I S T L P F R A D Y Y L R</u>	100
301	GGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGCTTATTCTGTATGTC	360
101	G S N W I F G D L A C R I M S Y S L Y V	120
361	AACATGTACAGCAGTATTATTCCTGACCGTGTGAGTGTGCGTTCTGGCAATG	420
121	<u>N M Y S S I Y F L T V L S V V R F L A M</u>	140
421	GTTCACCCCTTCGGCTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGG	480
141	<u>V H P F R L L H V T S I R S A W I L C G</u>	160
481	ATCATATGGATCCTTATCATGGCTCCTCAATAATGCTCTGGACAGTGGCTCTGAGCAG	540
161	<u>I I W I L I M A S S I M L L D S G S E Q</u>	180
541	AACGGCAGTGTACATCATGCTTAGAGCTGAATCTCTATAAAATTGCTAACAGTCAGACC	600
181	<u>N G S V T S C L E L N L Y K I A K L Q T</u>	200
601	ATGAACTATATTGCCATTGGTGGTGGCTGCCATTTCACACTCAGCATCTGT	660
201	<u>M N Y I A L V V G C L L P F F T L S I C</u>	220
661	TATCTGCTGATCATTGGGTTCTGTTAAAGTGGAGGTCCCAGAATGGGGCTGGGTT	720
221	<u>Y L L I I R V L L K V E V P E S G L R V</u>	240
721	TCTCACAGGAAGGCACtgaccaccatcatCACCTGATCATCTCTGTGTTTC	780
241	<u>S H R K A L T T I I I T L I I F F L C F</u>	260
781	CTGCCCTATCACACACTGAGGACCGTCCACTGACGACATGAAAGTGGGTTATGCAA	840
261	<u>L P Y H T L R T V H L T T W K V G L C K</u>	280
841	GACAGACTGCATAAGCTTGGTTATCACACTGGCCTGGCAGCAGCCAATGCCTGCTTC	900
281	<u>D R L H K A L V I T L A L A A A N A C F</u>	300

FIG. 2B

		251		300
HGPRBMY11	(217)	[REDACTED]	[REDACTED]	[REDACTED]
HGPRBMY11v1	(233)	[REDACTED]	[REDACTED]	[REDACTED]
P2Y5_CHICK	(213)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_CHICK	(238)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_MELGA	(238)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_RAT	(249)	[REDACTED]	[REDACTED]	[REDACTED]
Q9Y271	(221)	[REDACTED]	[REDACTED]	[REDACTED]
GPRH_HUMAN	(224)	[REDACTED]	[REDACTED]	[REDACTED]
		301		350
HGPRBMY11	(261)	[REDACTED]	[REDACTED]	[REDACTED]
HGPRBMY11v1	(277)	[REDACTED]	[REDACTED]	[REDACTED]
P2Y5_CHICK	(260)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_CHICK	(285)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_MELGA	(285)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_RAT	(296)	[REDACTED]	[REDACTED]	[REDACTED]
Q9Y271	(267)	[REDACTED]	[REDACTED]	[REDACTED]
GPRH_HUMAN	(269)	[REDACTED]	[REDACTED]	[REDACTED]
		351		379
HGPRBMY11	(311)	[REDACTED]	[REDACTED]	[REDACTED]
HGPRBMY11v1	(327)	[REDACTED]	[REDACTED]	[REDACTED]
P2Y5_CHICK	(306)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_CHICK	(335)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_MELGA	(335)	[REDACTED]	[REDACTED]	[REDACTED]
P2YR_RAT	(346)	[REDACTED]	[REDACTED]	[REDACTED]
Q9Y271	(316)	[REDACTED]	[REDACTED]	[REDACTED]
GPRH_HUMAN	(319)	[REDACTED]	[REDACTED]	[REDACTED]

P999142266 - P99914202

FIGURE 3. FTIR spectra

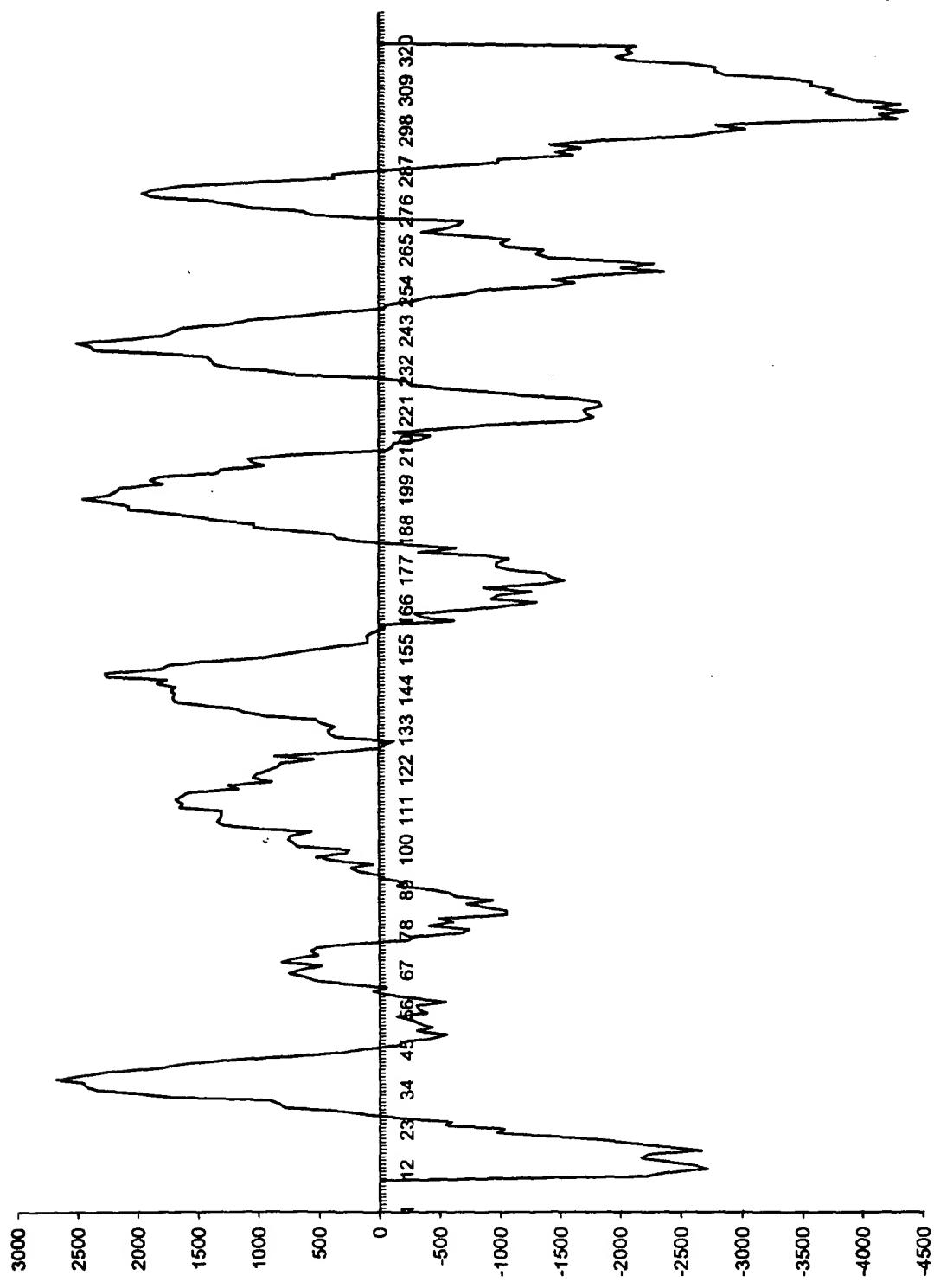


FIG. 3

FIG. 6B

901	AATCCTCTGCTCTATTACTTTGCTGGGGAGAATTTAAGGACAGACTAAAGTCTGCACTC	960
301	N P L L Y Y F A G E N F K D R L K S A L	320
961	AGAAAAGGCCATCCACAGAAGGCAAAGACAAAGTGTGTTCCCTGTTAGTGTGTGGTTG	1020
321	R K G H P Q K A K T K C V F P V S V W L	340
1021	AGAAAGGAAACAAGAGTATAA	1041
341	R K E T R V	346

FIG. 4

Expression Profiling of Novel Human GPCR, HGPRBMY11

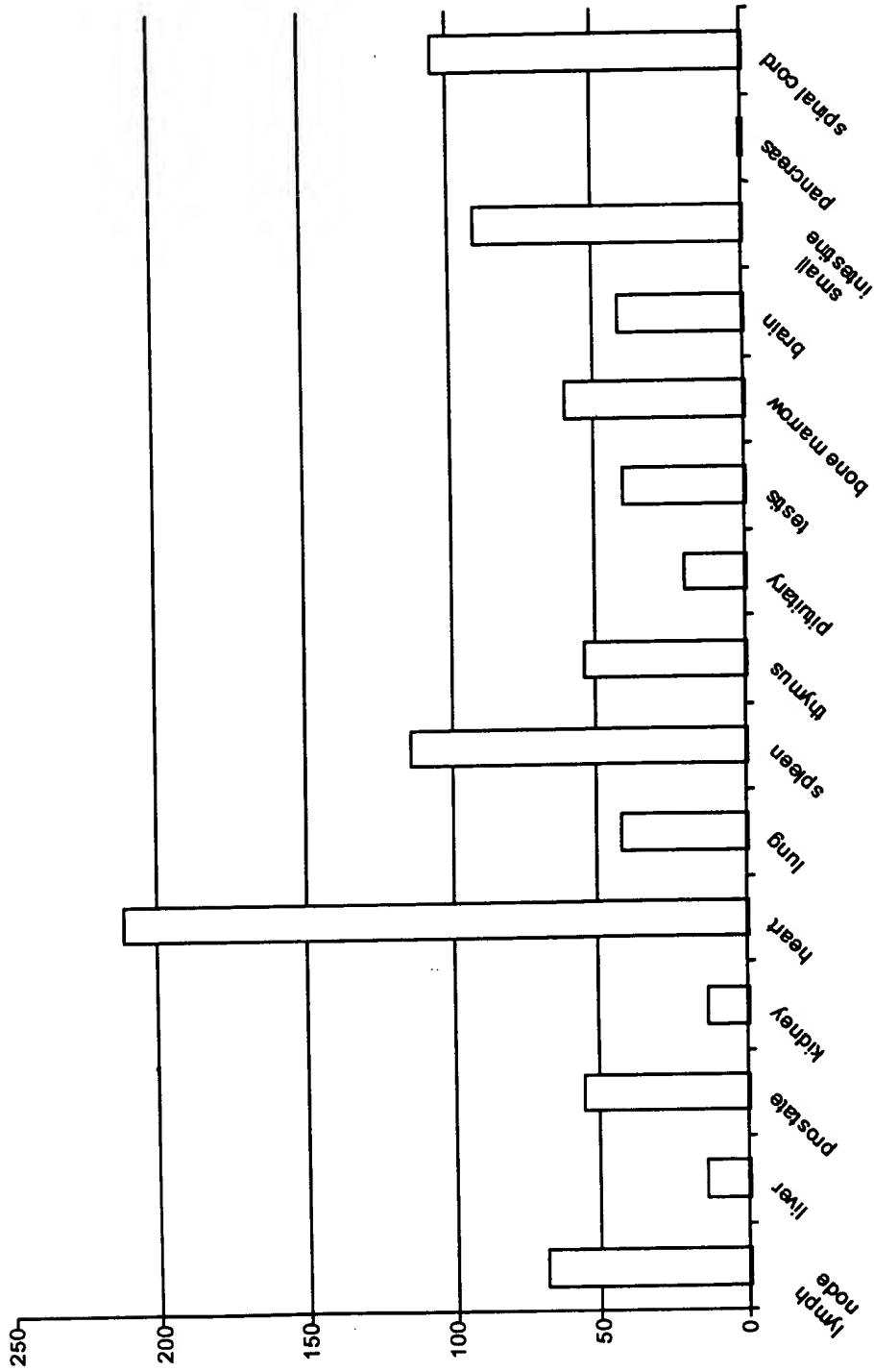


FIG. 5**HGPRBMY11**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37%	49%
chick purinergic receptor 5	gi P32250	36%	46%
human G-protein-coupled receptor GPR17	gi Q13304	36%	46%
chick purinergic receptor	gi P34996	30%	45%
turkey purinergic receptor	gi P49652	30%	45%
rat purinergic receptor	gi P49651	30%	44%

HGPRBMY11v1

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human cysteinyl leukotriene receptor	gi 11422069	37.2%	49%
chick purinergic receptor 5	gi P32250	36.7%	46.1%
human G-protein-coupled receptor GPR17	gi Q13304	36.2%	46.1%
chick purinergic receptor	gi P34996	29.5%	43.9%
turkey purinergic receptor	gi P49652	29.8%	44.2%
rat purinergic receptor	gi P49651	29.6%	44%

FIG. 7

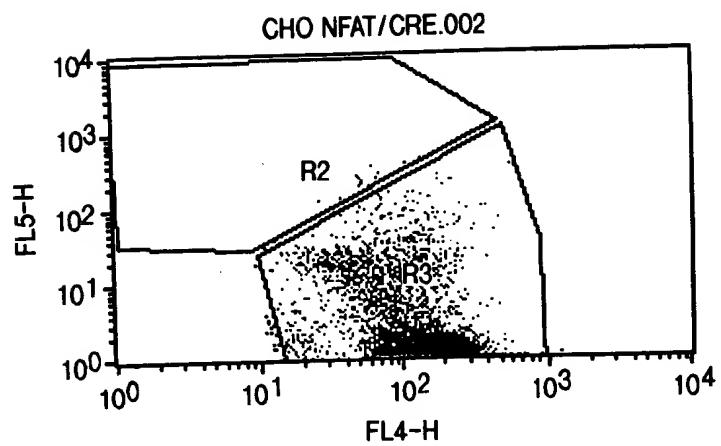


FIG. 8

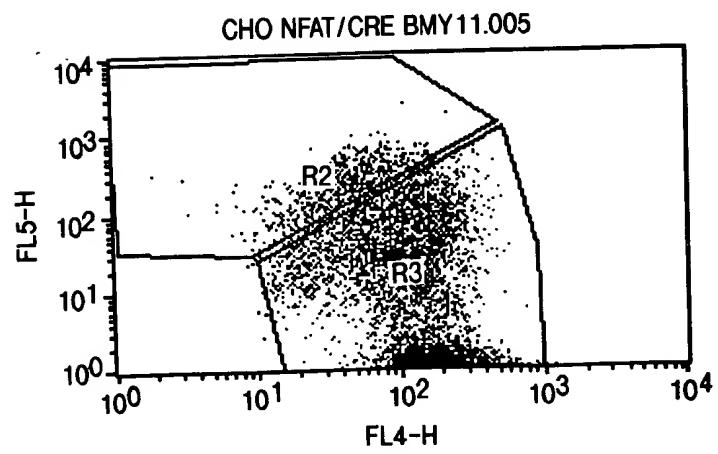


FIG. 9

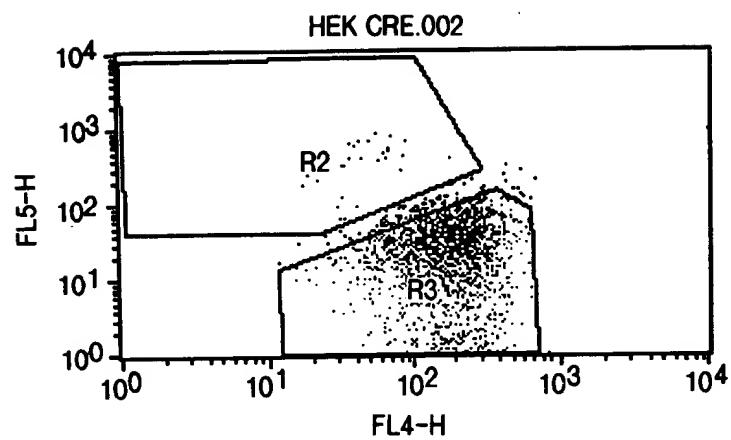


FIG. 10

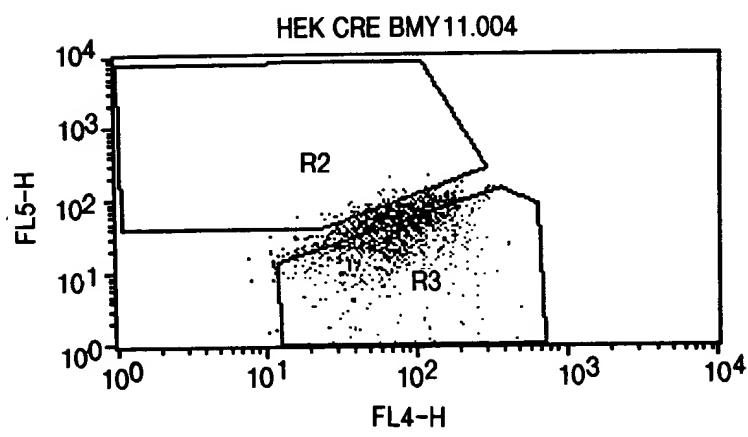


FIG. 11

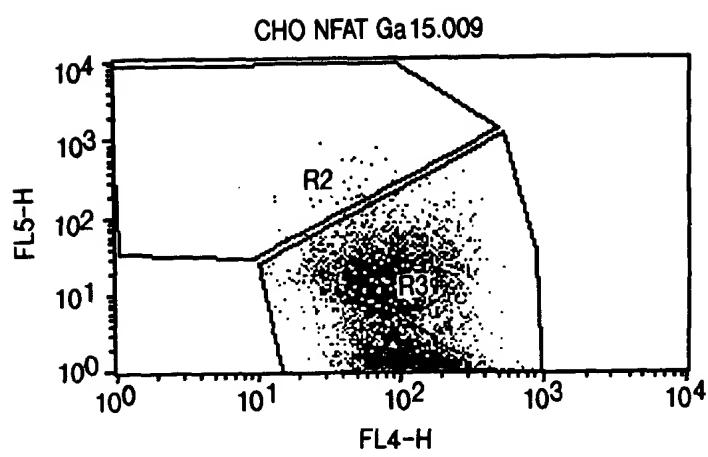


FIG. 12

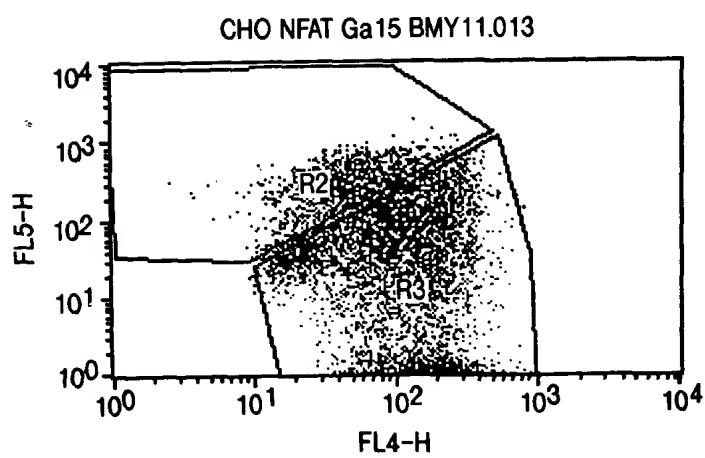
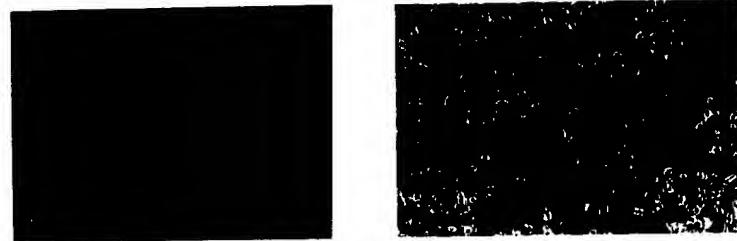


FIG. 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



Cho NFAT Ga15 BMY11 (Fluorescent vs. Bright Field)

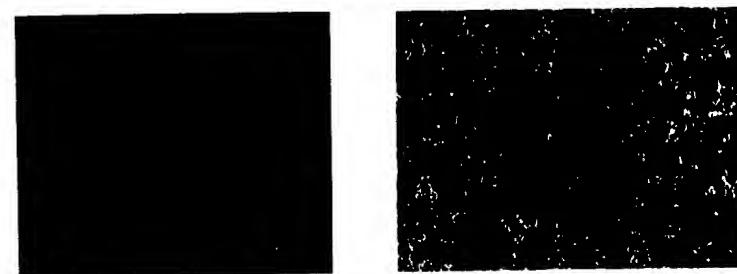


FIG. 14a

Cho-NFAT CRE

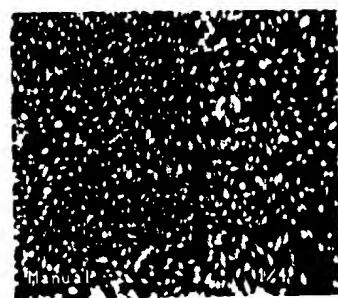


FIG. 14b

Cho-NFAT CRE + F/T/P

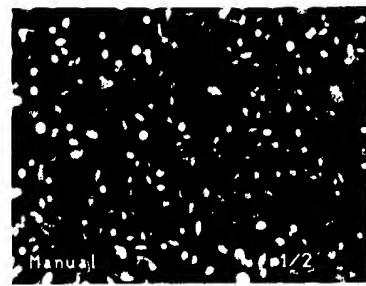


FIG. 14c

Cho-NFAT CRE oGPCR-Intermediate

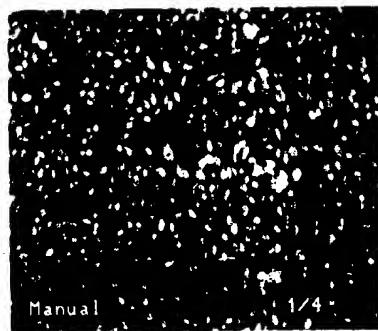


FIG. 14d

Cho-NFAT CRE oGPCR High

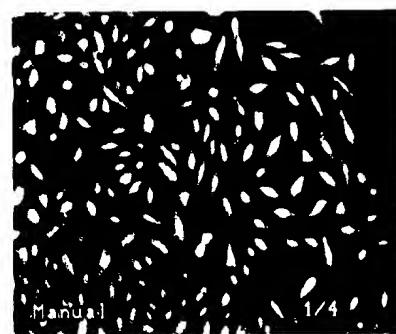


FIG. 15A

1	ATGTCCTTGCAACCACCATCCATCTCGTATCAGAAATGGAACCAAATGGCACCTTCAGCAAT	60
1	M S L Q P S I S V S E M E P N G T F S N	20
61	AACAACAGCAGGAAC TG CACAATTGAAAAC TT CAAGAGAGAATT T T C C A ATT GTAT AT	120
21	N N S R N C T I E N F K R E F F P I V Y	40
121	CTGATAATATTTCTGGGGACTCTGGAAATGGGTGTCCATATATGTTTCTGCAG	180
41	L I I F F W G V L G N G L S I Y V F L Q	60
181	CCTTATAAGAACATCTGTGAACGTTTCATGCTAAATCTGCCATTTCAGATCTC	240
61	P Y K K S T S V N V F M L N L A I S D L	80
241	CTGTTCATAGCACGCTTCCCTTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATA	300
81	L F I S T L P F R A D Y Y L R G S N W I	100
301	TTTGGAGACCTGGCCTGCAGGATTATGCTTATTCTGTATGTCAACATGTACAGCAGT	360
101	F G D L A C R I M S Y S L Y V N M Y S S	120
361	ATTTATTCCTGACCGTGCTGAGTGTGCGTTCTGGCAATGGTCACCCCTTCGG	420
121	I Y F L T V L S V V R F L A M V H P F R	140
421	CTTCTGCATGTCAACAGCATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT	480
141	L L H V T S I R S A W I L C G I I W I L	160
481	ATCATGGCTTCCCTCAATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCA	540
161	I M A S S I M L L D S G S E Q N G S V T	180
541	TCATGCTTAGAGCTGAATCTCTATAAAATTGCTAAGCTGCAGACCATGAACTATATTGCC	600
181	S C L E L N L Y K I A K L Q T M N Y I A	200
601	TTGGTGGTGGGCTGCCTGCTGCCATTTCACACTCAGCATCTGTTATCTGCTGATCATT	660
201	L V V G C L L P F F T L S I C Y L L I I	220
661	CGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCGGGCTGCGGGTTCTCACAGGAAGGCA	720
221	R V L L K V E V P E S G L R V S H R K A	240
721	CTGACCACCATCATCACCTTGATCATCTCTCTGTGTTCTGCCCTATCACACA	780
241	L T T I I T L I I F F L C F L P Y H T	260
781	CTGAGGACCGTCCACTTGACGACATGGAAAGTGGTTATGCAAAGACAGACTGCATAAA	840
261	L R T V H L T T W K V G L C K D R L H K	280
841	GCTTTGGTTATCACACTGGCCTGGCAGCAGCCAATGCCCTGCTCAATCCTCTGCTCTAT	900
281	A L V I T L A A A N A C F N P L L Y	300

FIG. 15B

901	TACTTGCTGGGAGAATTAAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCA	960
301	Y F A G E N F K D R L K S A L R K G H P	320
961	CAGAAGGCAAAGACAAAGTGTGTTCCCTGTTAGTGTGGTTGAGAAAGGAAACAAGA	1020
321	Q K A K T K C V F P V S V W L R K E T R	340
1021	GTATAA 1026	
341	V 341	